

10/03 5,368
updated search
L/cook 5/3/07

d his

(FILE 'HOME' ENTERED AT 11:52:35 ON 03 MAY 2007)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 11:53:08 ON 03
MAY 2007

L1 703 S (ANTIBOD? ARRAY)
L2 35045 S (CELL LYSATE)
L3 27 S L1 AND L2
L4 12 DUPLICATE REMOVE L3 (15 DUPLICATES REMOVED)
L5 9863 S L2 AND ANTIBOD?
L6 615 S L5 AND SCREEN?
L7 227 S L6 AND PD<1998
L8 0 S L7 AND SRRAY?
L9 0 S L7 AND ARRAY?
L10 0 S L7 AND CHIP?
L11 8327 S (BINDING PATTERN)
L12 0 S L11 AND L7
L13 14 S L11 AND L2
L14 5 DUPLICATE REMOVE L13 (9 DUPLICATES REMOVED)
L15 330 S (PROTEIN FINGERPRINTING)
L16 6 S L15 AND L2
L17 2 DUPLICATE REMOVE L16 (4 DUPLICATES REMOVED)
L18 10 S L7 AND PLATE?
L19 5 DUPLICATE REMOVE L18 (5 DUPLICATES REMOVED)
L20 62 S L7 AND ASSAY
L21 31 DUPLICATE REMOVE L20 (31 DUPLICATES REMOVED)
L22 31 S L21 AND PD<1998
L23 29 S L22 NOT L19
L24 990 S (ANTIBOD? PANEL)
L25 0 S L24 AND L2
L26 500 S L24 AND PD<1998
L27 6 S L26 AND L11

=>

DUPLICATE 2

AN 1989:515811 BIOSIS
 DN PREV198988131954; BA88:131954
 TI PROTEIN FINGERPRINTING A NOVEL VIRUS IDENTIFICATION SYSTEM.
 AU WALPITA P [Reprint author]; CONNOR J D; PFEIFER D
 CS DEP PEDIATR, M-009 E, UNIV CALIF, SAN DIEGO, LA JOLLA, CALIF 92093, USA
 SO Journal of Virological Methods, (1989) Vol. 25, No. 3, pp. 315-324.
 CODEN: JVMEHD. ISSN: 0166-0934.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 15 Nov 1989
 Last Updated on STN: 15 Nov 1989
 AB Viral proteins separated by one-dimensional SDS-PAGE produce protein binding patterns (fingerprints) which are unique for different viruses. We have applied this concept successfully for the development of a practical and objective virus identification system which is applicable to most viruses. The method is simple, specific, and, unlike the currently available methods, free from all virus-specific reagents. Interference by host protein bands in SDS-PAGE preparations of virus-infected cell lysates was eliminated consistently by treating virus infected cell cultures with optimum concentration of NaCl for selective inhibition of host protein synthesis. The method utilizes the comparison of protein fingerprints of 'unknown' viruses with protein fingerprints of reference viruses stored in a computer data base, using pattern recognition software. All 113 'unknown' virus strains were correctly identified to the genus level by the protein fingerprint method, when compared with the conventional virus identification methods.
 CC General biology - Information, documentation, retrieval and computer applications 00530
 Cytology - Animal 02506
 Biochemistry methods - Proteins, peptides and amino acids 10054
 Biophysics - Methods and techniques 10504
 Pathology - Diagnostic 12504
 Virology - General and methods 33502
 Virology - Animal host viruses 33506
 Medical and clinical microbiology - General and methods 36001
 Medical and clinical microbiology - Virology 36006
 IT Major Concepts
 Biochemistry and Molecular Biophysics; Computer Applications (Computational Biology); Infection; Methods and Techniques; Microbiology; Pathology
 IT Miscellaneous Descriptors
 COMPUTER DATA BASE PATTERN RECOGNITION SOFTWARE HOST PROTEIN INHIBITION
 SDS POLYACRYLAMIDE GEL ELECTROPHORESIS
 ORGN Classifier
 Viruses 03000
 Super Taxa
 Microorganisms
 Taxa Notes
 Microorganisms, Viruses

ANSWER 3 OF 5 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

DUPLICATE 2

AN 1989:515811 BIOSIS
DN PREV198988131954; BA88:131954
TI PROTEIN FINGERPRINTING A NOVEL VIRUS IDENTIFICATION SYSTEM.
AU WALPITA P [Reprint author]; CONNOR J D; PFEIFER D
CS DEP PEDIATR, M-009 E, UNIV CALIF, SAN DIEGO, LA JOLLA, CALIF 92093, USA
SO Journal of Virological Methods, (1989) Vol. 25, No. 3, pp. 315-324.
CODEN: JVMEHD. ISSN: 0166-0934.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 15 Nov 1989
Last Updated on STN: 15 Nov 1989
AB Viral proteins separated by one-dimensional SDS-PAGE produce protein binding patterns (fingerprints) which are unique for different viruses. We have applied this concept successfully for the development of a practical and objective virus identification system which is applicable to most viruses. The method is simple, specific, and, unlike the currently available methods, free from all virus-specific reagents. Interference by host protein bands in SDS-PAGE preparations of virus-infected cell lysates was eliminated consistently by treating virus infected cell cultures with optimum concentration of NaCl for selective inhibition of host protein synthesis. The method utilizes the comparison of protein fingerprints of 'unknown' viruses with protein fingerprints of reference viruses stored in a computer data base, using pattern recognition software. All 113 'unknown' virus strains were correctly identified to the genus level by the protein fingerprint method, when compared with the conventional virus identification methods.
CC General biology - Information, documentation, retrieval and computer applications 00530
Cytology - Animal 02506
Biochemistry methods - Proteins, peptides and amino acids 10054
Biophysics - Methods and techniques 10504
Pathology - Diagnostic 12504
Virology - General and methods 33502
Virology - Animal host viruses 33506
Medical and clinical microbiology - General and methods 36001
Medical and clinical microbiology - Virology 36006
IT Major Concepts
Biochemistry and Molecular Biophysics; Computer Applications (Computational Biology); Infection; Methods and Techniques; Microbiology; Pathology
IT Miscellaneous Descriptors
COMPUTER DATA BASE PATTERN RECOGNITION SOFTWARE HOST PROTEIN INHIBITION
SDS POLYACRYLAMIDE GEL ELECTROPHORESIS
ORGN Classifier
Viruses 03000
Super Taxa
Microorganisms
Taxa Notes
Microorganisms, Viruses

ANSWER 15 OF 29 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1985:421101 CAPLUS
DN 103:21101
ED Entered STN: 27 Jul 1985
TI Assay for monoclonal antibody against surface Ig of a
human B cell tumor
IN Levy, Ronald; Maloney, David G.; Thielemans, Kristiaan
PA Leland Stanford Junior University, USA
SO U.S., 10 pp.
CODEN: USXXAM
DT Patent
LA English
IC ICM G01N033-54
INCL 436518000
CC 15-1 (Immunochemistry)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 4513088	A	19850423	US 1983-480478	19830330 <--
PRAI	US 1983-480478		19830330		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 4513088	ICM	G01N033-54
	INCL	436518000
	IPCI	G01N0033-54 [ICM,3]
	IPCR	G01N0033-574 [I,C*]; G01N0033-574 [I,A]; G01N0033-68 [I,C*]; G01N0033-68 [I,A]
	NCL	435/007.230; 435/004.000; 435/007.500; 435/007.920; 435/028.000; 435/259.000; 435/948.000; 435/965.000; 435/969.000; 436/518.000; 436/528.000; 436/531.000; 436/548.000; 436/804.000; 436/813.000; 436/823.000

AB An assay that facilitates screening of hybridoma culture media for monoclonal anti-idiotypic antibodies, particularly murine monoclonal antibodies that are useful for treating human B cell tumors is disclosed. The assay is a solid phase type assay and involves: incubating a lysate of the patient's B cell tumor with immobilized antihuman Ig, separating unbound lysate materials, incubating the remaining immobilized complex with the test culture medium, separating unbound culture medium material, and incubating the remaining immobilized complex with a labeled anti-mouse Ig, separating unbound labeled anti-mouse Ig, and detecting the presence of label in the remaining immobilized complex. Thus, the sera of 10 patients with B cell tumors were analyzed. The idiotypes of 8 patients were IgM, whereas those of the other 2 were IgG. In addition, 5 monoclonal anti-idiotypes used in the assay reacted only with their corresponding tumor cell lysates and not with lysates of other patients.

ST monoclonal antibody detn B lymphocyte tumor

IT Enzymes

RL: BIOL (Biological study)
(in detection of antibodies to surface Igs of B-cell tumors of human)

IT Neoplasm, composition
(surface Igs of, antibodies to, detection of, by immunoassay, of humans with B-cell tumor)

IT Immunoglobulins
RL: PROC (Process)
(to surface Ig of B cell tumor of human, detection of, by immunoassay)

IT Lymphocyte
(B-, surface Igs of tumors of, antibodies to, detection of, by immunoassay, of human)

IT Lymphoma
(B-cell, surface Igs of human, antibodies to, detection of, by immunoassay)

ANSWER 15 OF 29 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1985:421101 CAPLUS

DN 103:21101

ED Entered STN: 27 Jul 1985

TI Assay for monoclonal antibody against surface Ig of a human B cell tumor

IN Levy, Ronald; Maloney, David G.; Thielemans, Kristiaan

PA Leland Stanford Junior University, USA

SO U.S., 10 pp.

CODEN: USXXAM

DT Patent

LA English

IC ICM G01N033-54

INCL 436518000

CC 15-1 (Immunochemistry)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 4513088	A	19850423	US 1983-480478	19830330 <--
PRAI	US 1983-480478		19830330		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 4513088	ICM	G01N033-54
	INCL	436518000
	IPCI	G01N0033-54 [I,C*]
	IPCR	G01N0033-574 [I,C*]; G01N0033-574 [I,A]; G01N0033-68 [I,C*]; G01N0033-68 [I,A]
	NCL	435/007.230; 435/004.000; 435/007.500; 435/007.920; 435/028.000; 435/259.000; 435/948.000; 435/965.000; 435/969.000; 436/518.000; 436/528.000; 436/531.000; 436/548.000; 436/804.000; 436/813.000; 436/823.000

AB An assay that facilitates screening of hybridoma culture media for monoclonal anti-idiotypic antibodies, particularly murine monoclonal antibodies that are useful for treating human B cell tumors is disclosed. The assay is a solid phase type assay and involves: incubating a lysate of the patient's B cell tumor with immobilized antihuman Ig, separating unbound lysate materials, incubating the remaining immobilized complex with the test culture medium, separating unbound culture medium material, and incubating the remaining immobilized complex with a labeled anti-mouse Ig, separating unbound labeled anti-mouse Ig, and detecting the presence of label in the remaining immobilized complex. Thus, the sera of 10 patients with B cell tumors were analyzed. The idiotypes of 8 patients were IgM, whereas those of the other 2 were IgG. In addition, 5 monoclonal anti-idiotypes used in the assay reacted only with their corresponding tumor cell lysates and not with lysates of other patients.

ST monoclonal antibody detn B lymphocyte tumor

IT Enzymes

RL: BIOL (Biological study)

(in detection of antibodies to surface Igs of B-cell tumors of human)

IT Neoplasm, composition

(surface Igs of, antibodies to, detection of, by immunoassay, of humans with B-cell tumor)

IT Immunoglobulins

RL: PROC (Process)

(to surface Ig of B cell tumor of human, detection of, by immunoassay)

IT Lymphocyte

(B-, surface Igs of tumors of, antibodies to, detection of, by immunoassay, of human)

IT Lymphoma

(B-cell, surface Igs of human, antibodies to, detection of, by immunoassay)

IT Immunoglobulins
RL: PROC (Process)
(G, to surface Ig of B cell tumor of human, detection of, by
immunoassay)

IT Immunoglobulins
RL: PROC (Process)
(M, to surface Ig of B cell tumor of human, detection of, by
immunoassay)

IT Immunochemical analysis
(immunoassay, antibodies to surface Igs of B-cell tumors of
human detection in).

IT Immunoglobulins
RL: PROC (Process)
(G, to surface Ig of B cell tumor of human, detection of, by
immunoassay)

IT Immunoglobulins
RL: PROC (Process)
(M, to surface Ig of B cell tumor of human, detection of, by
immunoassay)

IT Immunochemical analysis
(immunoassay, antibodies to surface Igs of B-cell tumors of
human detection in)

d his

(FILE 'HOME' ENTERED AT 11:52:35 ON 03 MAY 2007)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 11:53:08 ON 03 MAY 2007

L1 703 S (ANTIBOD? ARRAY)
L2 35045 S (CELL LYSATE)
L3 27 S L1 AND L2
L4 12 DUPLICATE REMOVE L3 (15 DUPLICATES REMOVED)
L5 9863 S L2 AND ANTIBOD?
L6 615 S L5 AND SCREEN?
L7 227 S L6 AND PD<1998
L8 0 S L7 AND SRRAY?
L9 0 S L7 AND ARRAY?
L10 0 S L7 AND CHIP?
L11 8327 S (BINDING PATTERN)
L12 0 S L11 AND L7
L13 14 S L11 AND L2
L14 5 DUPLICATE REMOVE L13 (9 DUPLICATES REMOVED)
L15 330 S (PROTEIN FINGERPRINTING)
L16 6 S L15 AND L2
L17 2 DUPLICATE REMOVE L16 (4 DUPLICATES REMOVED)
L18 10 S L7 AND PLATE?
L19 5 DUPLICATE REMOVE L18 (5 DUPLICATES REMOVED)
L20 62 S L7 AND ASSAY
L21 31 DUPLICATE REMOVE L20 (31 DUPLICATES REMOVED)
L22 31 S L21 AND PD<1998
L23 29 S L22 NOT L19
L24 990 S (ANTIBOD? PANEL)
L25 0 S L24 AND L2
L26 500 S L24 AND PD<1998
L27 6 S L26 AND L11

=>

UniProtKB/TrEMBL entry Q4KNZ8

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#)

[\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	Q4KNZ8_9BURK
Primary accession number	Q4KNZ8
Secondary accession numbers	None
Integrated into TrEMBL on	August 2, 2005
Sequence was last modified on	September 5, 2006 (Sequence version 2)
Annotations were last modified on	April 3, 2007 (Entry version 11)

Name and origin of the protein

Protein name	Hydroxysimazine hydrolase
Synonyms	None
Gene name	Name: smzB
From	Herbaspirillum sp. B601 [TaxID: 321700]
Encoded on	Plasmid pHB1.
Taxonomy	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Herbaspirillum.

References

- [1] NUCLEOTIDE SEQUENCE.
STRAIN=B601;
Bazhanov D.P., Zabenkova C.I., Yatsevitch K.K., Bazhanova A.A., Yarmolinsky D.G.;
"Simazine-Degrading Herbaspirillum sp. Isolated from Maize Roots in Belarus."
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
- [2] NUCLEOTIDE SEQUENCE.
STRAIN=B601;
Yatsevich K.K., Bazhanov D.P., Yarmolinsky D.G.;
Submitted (AUG-2006) to the EMBL/GenBank/DDBJ databases.

Comments

Copyright

Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.

Cross-references

Sequence databases

EMBL AY965854; AAY40323.2; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases

ModBase Q4KNZ8.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Ontologies

GO

GO:0016787; Molecular function: hydrolase activity (inferred from electronic annotation from UniProtKB-KW).

QuickGo view.

Family and domain databases

InterPro

IPR006680; Amidohydro_1.
IPR011059; Metal-dep_hydro_comp.
Graphical view of domain structure.

Gene3D

G3DSA:1.20.800.10; G3DSA:1.20.800.10; 1.

Pfam

PF01979; Amidohydro_1; 1.
Pfam graphical view of domain structure.

ProDom

[Domain structure / List of seq. sharing at least 1 domain]

Other

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Hydrolase; Plasmid.

Features

None

Sequence information

Length: 481 AA

Molecular weight: 52171 Da

CRC64: CC3EF0F08E1CDA91 [This is a checksum on the sequence]

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MTTTLTYTGFH	QLVTGDVAGT	VLNGVDILVR	DGEIIGLGPD	LPRTLAPIGV	GQEQGVEEVN
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
CRGLTAYPGL	INTHHHFFQA	FVRNLAPLDW	TQLDVLAWLR	KIYPVFALVD	EDCIYHSTVV
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
SMAELIKHGC	TTAFDHQYNY	SRRGGPFLVD	RQFDAANLLG	LRFHAGRGCI	TLPMAEGSTI
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
PDAMRESTDT	FLADCERLVS	RFHDPRPFAM	QRVVVAPCQP	VIAYPETFVE	SARLARHLGV
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
SLHTHLGEGE	TPAMVARFGE	RSLDWCENRG	FVGPDVWLAH	GWEFTAADIA	RLAATGTGVA
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
HCPAPVFLVG	AEVTDIPAMA	AAGVRVGFGV	DGHASNDSSN	LAECIRLAYL	LQCLKASERQ
<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>	<u>410</u>	<u>420</u>
HPVPAPYDFL	RMATQGGADC	LNRPDLGALA	VGRAADFFAV	DLNRIEYIGA	NHDPRSLPAK
<u>430</u>	<u>440</u>	<u>450</u>	<u>460</u>	<u>470</u>	<u>480</u>

VGFSGPVDMT VINGKVVRN GEFPGLEME LARAADGVFR RVIYGDPLVA ALRRGTGVTP

C

Q4KNZ8 in FAST/
format[View entry in original UniProtKB/TrEMBL format](#)[View entry in raw text format \(no links\)](#)[Request for annotation of this UniProtKB/TrEMBL entry](#)**BLAST**BLAST submission on
ExPASy/SIB
or at NCBI (USA)Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-
MODELNPSA Sequence analysis
tools[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)Hosted by  CBR Canada Mirror sites: Australia Brazil China Korea Switzerland

UniProtKB/Swiss-Prot entry P72156

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features]

[Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	ATZA_PSESD
Primary accession number	P72156
Secondary accession numbers	None
Integrated into Swiss-Prot on	July 15, 1998
Sequence was last modified on	May 30, 2000 (Sequence version 2)
Annotations were last modified on	May 1, 2007 (Entry version 43)

Name and origin of the protein

Protein name	Atrazine chlorohydrolase
Synonym	EC 3.8.1.8
Gene name	Name: atzA
From	Pseudomonas sp. (strain ADP) [TaxID: 47660]
Encoded on	Plasmid pADP-1.
Taxonomy	Bacteria; Proteobacteria.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PROTEIN SEQUENCE OF 1-10.
PubMed=8759853 [NCBI, ExPASy, EBI, Israel, Japan]
de Souza M.L., Sadowsky M.J., Wackett L.P.;
"Atrazine chlorohydrolase from Pseudomonas sp. strain ADP: gene sequence, enzyme purification, and protein characterization.";
J. Bacteriol. 178:4894-4900(1996).

[2] SEQUENCE REVISION TO 335 AND 400-406.
de Souza M.L., Sadowsky M.J., Wackett L.P.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

[3] CHARACTERIZATION OF METAL REQUIREMENT.
DOI=10.1021/bi020415s; PubMed=12450410 [NCBI, ExPASy, EBI, Israel, Japan]
Seffernick J.L., McTavish H., Osborne J.P., de Souza M.L., Sadowsky M.J., Wackett L.P.;
"Atrazine chlorohydrolase from Pseudomonas sp. strain ADP is a metalloenzyme.";
Biochemistry 41:14430-14437(2002).

Comments

- FUNCTION:** Hydrolytically dechlorinates atrazine to hydroxyatrazine. Dechlorinates also simazine, and desethylatrazine but is not active with melamine, terbutylazine, or desethyldeisopropylatrazine.

- **CATALYTIC ACTIVITY:** Atrazine + H₂O = 4-(ethylamino)-2-hydroxy-6-(isopropylamino)-1,3,5-triazine + HCl.
- **COFACTOR:** Fe(2+).
- **PATHWAY:** Atrazine degradation; first step.
- **SUBUNIT:** Homotetramer.
- **SUBCELLULAR LOCATION:** Cytoplasm (*Potential*).
- **SIMILARITY:** Belongs to the ATZ/TRZ family.

Copyright

Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.

Cross-references

Sequence databases

EMBL U55933; AAC64663.1; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR T47197; T47197.

3D structure databases

ModBase P72156.

Enzyme and pathway databases

BioCyc MetaCyc:MONOMER-901; -.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Ontologies

GO GO:0018788; Molecular function: atrazine chlorohydrolase activity (*inferred from electronic annotation from EC*).
QuickGo view.

Family and domain databases

InterPro IPR006680; Amidohydro_1.
IPR011550; Amidohydro_like.
IPR011059; Metal-dep_hydro_comp.
Graphical view of domain structure.
Gene3D G3DSA:3.20.20.140; G3DSA:3.20.20.140; 1.
Pfam PF01979; Amidohydro_1; 1.
Pfam graphical view of domain structure.
ProDom PD001248; Amidohydro_like; 1.
[Domain structure / List of seq. sharing at least 1 domain]
BLOCKS P72156.

Other

ProtoNet P72156.
UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Direct protein sequencing; Hydrolase; Iron; Plasmid.

Features



Feature table viewer

Key	From	To	Length	Description	FTId
CHAIN	1	474	474	Atrazine chlorohydrolase.	PRO_0000122293

Sequence information

Length: **474 AA** [This is the length of the unprocessed precursor]

Molecular weight: **52486 Da** [This is the MW of the unprocessed precursor]

CRC64: **51C1F6C755F141D4** [This is a checksum on the sequence]

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MQTLSIQHGT	LVTMDQYRRV	LGDSWVHVQD	GRIVALGVHA	ESVPPPADRV	IDARGKVVL
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
GFINAHTHVN	QILLRGGPSH	GRQFYDWLFN	VVYPGQKAMR	PEDVAVAVRL	YCAEAVRSGI
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
TTINENADSA	IYPGNIEAAM	AVYGEVGVRV	VYARMFFDRM	DGRIQGYVDA	LKARSPQVEL
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
CSIMEETAVA	KDRITALSDQ	YHGTAAGRIS	VWPAPATTTA	VTVEGMRWAQ	AFARDRAVMW
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
TLHMAESDHD	ERIHGMSPAE	YMECYGLLDE	RLQVAHCVFY	DRKDVRLLRH	HNVKVASQVV
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
SNAYLGSGVA	PVPPEMVERGM	AVGIGTDNGN	SNDSVNMIGD	MKFMAHIHRA	VHRDADVLT
<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>	<u>410</u>	<u>420</u>
EKILEMATID	GARSLGMDHE	IGSIETGKRA	DLILLDLRHP	QTTPHHHLAA	TIVFQAYGNE
<u>430</u>	<u>440</u>	<u>450</u>	<u>460</u>	<u>470</u>	
VDTVLIIDGNV	VMENRRLSFL	PPERELAFLE	EAQSRATAIL	QRANMVANPA	WRSL

P72156 in FASTA format

View entry in original UniProtKB/Swiss-Prot format

View entry in raw text format (no links)

Report form for errors/updates in this UniProtKB/Swiss-Prot entry

BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL



NPSA Sequence analysis tools



ExPASy Home page

Site Map

Search ExPASy

Contact us

Swiss-Prot

Hosted by CBR Canada Mirror sites: Australia Brazil China Korea Switzerland

Search for

[Printer-friendly view](#)

[Request update](#)

[Quick BlastP search](#)

[Entry history](#)

UniProtKB/TrEMBL entry A0MLT0

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#)
[\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	A0MLT0_9MICC
Primary accession number	A0MLT0
Secondary accession numbers	None
Integrated into TrEMBL on	December 12, 2006
Sequence was last modified on	December 12, 2006 (Sequence version 1)
Annotations were last modified on	February 6, 2007 (Entry version 2)

Name and origin of the protein

Protein name	Triazine hydrolase
Synonyms	None
Gene name	None
From	Arthrobacter sp. AD25 [TaxID: 282184]
Taxonomy	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.

References

[1] NUCLEOTIDE SEQUENCE.
Li Y., Cai B.;
"The development of a high efficiency atrazine-degrading bacterium by plasmid-assisted molecular breeding."
Submitted (SEP-2006) to the EMBL/GenBank/DDBJ databases.

Comments

Copyright

Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.

Cross-references

Sequence databases

EMBL DQ989289; ABK41867.1; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases

ModBase A0MLT0.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Ontologies

GO

GO:0016787; Molecular function: hydrolase activity (inferred from electronic annotation from UniProtKB-KW).

QuickGo view.

Family and domain databases

ProDom

[Domain structure / List of seq. sharing at least 1 domain]

Other

UniRef

View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Hydrolase.

Features

None

Sequence information

Length: 456 AA

Molecular weight: 49838 Da

CRC64: 6113DCAA255C2278 [This is a checksum on the sequence]

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MILIRGLTRV	ITFDDQEREL	EDADILIDGP	KIVAVGKDLS	DRSVSRTIDG	RGMIALPGLI
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
NSHQHLYEGA	MRAIPQLERV	TMASWLEGVL	TRSAGWWRDG	KFGPDVIREV	ARAVLLESLL
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
GGITTVADQH	LFFPGATADS	YIDATIEAAT	DLGIRFHAAR	SSMTLGKSEG	GFCDDLFEVP
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
VDRVVQHCLG	LIDQYHEPEP	FGMVRIALEP	CGVPYDKPEL	FEAFAQMAAD	YDVRLHTHFY
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
EPLDAGMSDH	LYGMTPWRF	EKHGWASDRV	WLAHAVVPPR	EEIPEFADAG	VAIAHLIAPD
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
LRLGWGLAPI	REYLDAGITV	GFGTTGSASN	DGGNLLGDLR	LAALAHRPAD	PNEPEKWLSA
<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>	<u>410</u>	<u>420</u>
RELLRMATRG	SAECLGRPDL	GVLEEGRAD	IACWRLDGVD	RVGVHDP	PAIGLIMTGLSDRA
<u>430</u>	<u>440</u>	<u>450</u>			
SLVVVNGQVL	VENERPVLAD	LERIVANTTA	LIPKNL		

A0MLT0 in FAST/ format

View entry in original UniProtKB/TrEMBL format

View entry in raw text format (no links)

Request for annotation of this UniProtKB/TrEMBL entry

BLAST

BLAST submission on ExPASy/SIB or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL



NPSA Sequence analysis tools




ExPASy Home page

Site Map

Search ExPASy

Contact us

Swiss-Prot

Hosted by  CBR Canada Mirror sites: Australia Brazil China Korea Switzerland